Tuomas A Heikkinen

List of Publications by Year
in descending order

68	7,912	101496 36	95218 68
papers	citations	h-index	g-index

68	68	68	12212
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	0.8	270
2	3â€²RNA Sequencing Accurately Classifies Formalin-Fixed Paraffin-Embedded Uterine Leiomyomas. Cancers, 2020, 12, 3839.	1.7	9
3	Recurrent moderateâ€risk mutations in Finnish breast and ovarian cancer patients. International Journal of Cancer, 2019, 145, 2692-2700.	2.3	19
4	MED12 mutations and fumarate hydratase inactivation in uterine adenomyomas. Human Reproduction Open, 2018, 2018, hoy020.	2.3	5
5	Mediator Kinase Disruption in MED12-Mutant Uterine Fibroids From Hispanic Women of South Texas. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4283-4292.	1.8	20
6	Somatic MED12 Nonsense Mutation Escapes mRNA Decay and Reveals a Motif Required for Nuclear Entry. Human Mutation, 2017, 38, 269-274.	1.1	20
7	Exome Sequencing of Uterine Leiomyosarcomas Identifies Frequent Mutations in TP53, ATRX, and MED12. PLoS Genetics, 2016, 12, e1005850.	1.5	94
8	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
9	Somatic MED12 mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. Prostate, 2016, 76, 22-31.	1.2	33
10	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
11	MED12 mutations and FH inactivation are mutually exclusive in uterine leiomyomas. British Journal of Cancer, 2016, 114, 1405-1411.	2.9	43
12	SomaticMED12mutations are associated with poor prognosis markers in chronic lymphocytic leukemia. Oncotarget, 2015, 6, 1884-1888.	0.8	49
13	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
14	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
15	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
16	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
17	Breast-Cancer Risk in Families With Mutations in PALB2. Obstetrical and Gynecological Survey, 2014, 69, 659-660.	0.2	1
18	Evaluation of the RHINO gene for breast cancer predisposition in Finnish breast cancer families. Breast Cancer Research and Treatment, 2014, 144, 437-441.	1.1	1

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19	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
20	Polymorphisms in oxidative stress-related genes and mortality in breast cancer patients â€“ Potential differential effects by radiotherapy?. Breast, 2013, 22, 817-823.	0.9	31
21	Identification of genetic markers with synergistic survival effect in cancer. BMC Systems Biology, 2013, 7, S2.	3.0	1
22	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2013, 132, 2044-2055.	2.3	11
23	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
24	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
25	Eukaryotic translation initiation factor 4E (eIF4E) expression is associated with breast cancer tumor phenotype and predicts survival after anthracycline chemotherapy treatment. Breast Cancer Research and Treatment, 2013, 141, 79-88.	1.1	33
26	Overabundant FANCD2, alone and combined with NQO1, is a sensitive marker of adverse prognosis in breast cancer. Annals of Oncology, 2013, 24, 2780-2785.	0.6	28
27	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	1.1	513
28	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.3	8
29	Utilization of fluorescence in situ hybridization with cytokeratin discriminators in TOP2A assessment of chemotherapy-treated patients with breast cancer. Human Pathology, 2012, 43, 1363-1375.	1.1	2
30	Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. PLoS ONE, 2012, 7, e35706.	1.1	11
31	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
32	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
33	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	1.4	152
34	Genetic variation of ESR1 and its co-activator PPARGC1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. Breast Cancer Research, 2011, 13, R10.	2.2	15
35	Exploring the link between MORF4L1 and risk of breast cancer. Breast Cancer Research, 2011, 13, R40.	2.2	23
36	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	2.2	71

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37	Variants on the promoter region of PTEN affect breast cancer progression and patient survival. Breast Cancer Research, 2011, 13, R130.	2.2	43
38	Data Integration Workflow for Search of Disease Driving Genes and Genetic Variants. PLoS ONE, 2011, 6, e18636.	1.1	4
39	Glycodelin expression associates with differential tumour phenotype and outcome in sporadic and familial non-BRCA1/2 breast cancer patients. Breast Cancer Research and Treatment, 2011, 128, 85-95.	1.1	17
40	A combined analysis of genome-wide association studies in breast cancer. Breast Cancer Research and Treatment, 2011, 126, 717-727.	1.1	90
41	Common Genetic Variation at BARD1 Is Not Associated with Breast Cancer Risk in BRCA1 or BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1032-1038.	1.1	16
42	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	1.4	71
43	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	3.2	47
44	7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. Journal of Medical Genetics, 2011, 48, 698-702.	1.5	5
45	RAD51C is a susceptibility gene for ovarian cancer. Human Molecular Genetics, 2011, 20, 3278-3288.	1.4	124
46	Interplay between BRCA1 and RHAMM Regulates Epithelial Apicobasal Polarization and May Influence Risk of Breast Cancer. PLoS Biology, 2011, 9, e1001199.	2.6	91
47	MiR-34a Expression Has an Effect for Lower Risk of Metastasis and Associates with Expression Patterns Predicting Clinical Outcome in Breast Cancer. PLoS ONE, 2011, 6, e26122.	1.1	70
48	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
49	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	9.4	309
50	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	1.1	33
51	Multi-Variant Pathway Association Analysis Reveals the Importance of Genetic Determinants of Estrogen Metabolism in Breast and Endometrial Cancer Susceptibility. PLoS Genetics, 2010, 6, e1001012.	1.5	41
52	Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. PLoS Medicine, 2010, 7, e1000279.	3.9	764
53	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptorâ€“Negative Breast Cancer Survival. Journal of the National Cancer Institute, 2010, 102, 650-662.	3.0	48
54	A genome-wide association scan on estrogen receptor-negative breast cancer. Breast Cancer Research, 2010, 12, R93.	2.2	35

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55	Evidence for SMAD3 as a modifier of breast cancer risk in BRCA2mutation carriers. Breast Cancer Research, 2010, 12, R102.	2.2	25
56	Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. Breast Cancer Research, 2010, 12, R50.	2.2	18
57	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	1.4	84
58	Risk of Estrogen Receptorâ€“Positive and â€“Negative Breast Cancer and Singleâ€“Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	3.0	99
59	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	1.4	99
60	The Breast Cancer Susceptibility Mutation PALB2 1592delT Is Associated with an Aggressive Tumor Phenotype. Clinical Cancer Research, 2009, 15, 3214-3222.	3.2	122
61	No evidence that GATA3 rs570613 SNP modifies breast cancer risk. Breast Cancer Research and Treatment, 2009, 117, 371-379.	1.1	12
62	Germ-line variation at a functional p53 binding site increases susceptibility to breast cancer development. The HUGO Journal, 2009, 3, 31-40.	4.1	5
63	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
64	Evaluation of a candidate breast cancer associated SNP in ERCC4 as a risk modifier in BRCA1 and BRCA2 mutation carriers. Results from the Consortium of Investigators of Modifiers of BRCA1/BRCA2 (CIMBA). British Journal of Cancer, 2009, 101, 2048-2054.	2.9	15
65	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	1.1	57
66	An evaluation of the polymorphisms Ins16bp and Arg72Pro in p53 as breast cancer risk modifiers in BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2008, 99, 974-977.	2.9	14
67	Aberrations of the MRE11â€“RAD50â€“NBS1 DNA damage sensor complex in human breast cancer: MRE11 as a candidate familial cancerâ€predisposing gene. Molecular Oncology, 2008, 2, 296-316.	2.1	147
68	BARD1 variants Cys557Ser and Val507Met in breast cancer predisposition. European Journal of Human Genetics, 2006, 14, 167-172.	1.4	41